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RAW SEQUENCE LISTING

DATE: 07/12/2002

PATENT APPLICATION: US/09/674,035A

TIME: 10:40:08

Input Set : A:\227274078.ST25.txt

Output Set: N:\CRF3\07122002\I674035A.raw

3 <110> APPLICANT: Lang, Jas C.
 5 <120> TITLE OF INVENTION: Detecting the Expression of the DESC1 Gene in Squamous Cell Carcinoma

7 <130> FILE REFERENCE: 22727/04078
 9 <140> CURRENT APPLICATION NUMBER: 09/674,035A
 10 <141> CURRENT FILING DATE: 2000-12-11
 12 <150> PRIOR APPLICATION NUMBER: PCT/IB99/01818
 13 <151> PRIOR FILING DATE: 1999-11-11
 15 <160> NUMBER OF SEQ ID NOS: 10
 17 <170> SOFTWARE: PatentIn version 3.1
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 1269
 21 <212> TYPE: DNA
 22 <213> ORGANISM: DESC1
 24 <220> FEATURE:
 25 <221> NAME/KEY: CDS
 26 <222> LOCATION: (1)..(1269)
 27 <223> OTHER INFORMATION:
 30 <400> SEQUENCE: 1

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33 1 5 10 15	
35 ccc tgg gtt atc ggc ctc gtc atc ttc ata tcc ctg att gtc ctg gca	96
36 Pro Trp Val Ile Gly Leu Val Ile Phe Ile Ser Leu Ile Val Leu Ala	
37 20 25 30	
39 gtg tgc att gga ctc act gtt cat tat gtg aga tat aat caa aag aag	144
40 Val Cys Ile Gly Leu Thr Val His Tyr Val Arg Tyr Asn Gln Lys Lys	
41 35 40 45	
43 acc tac aat tac tat agc aca ttg tca ttt aca act gac aaa cta tat	192
44 Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr Thr Asp Lys Leu Tyr	
45 50 55 60	
47 gct gag ttt ggc aga gag gct tct aac aat ttt aca gaa atg agc cag	240
48 Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn Phe Thr Glu Met Ser Gln	
49 65 70 75 80	
51 aga ctt gaa tca atg gtg aaa aat gca ttt tat aaa tct cca tta agg	288
52 Arg Leu Glu Ser Met Val Lys Asn Ala Phe Tyr Lys Ser Pro Leu Arg	
53 85 90 95	
55 gaa gaa ttt gtc aag tct cag gtt atc aag ttc agt caa cag aag cat	336
56 Glu Glu Phe Val Lys Ser Gln Val Ile Lys Phe Ser Gln Gln Lys His	
57 100 105 110	
59 gga gtg ttg gct cat atg ctg ttg att tgt aga ttt cac tct act gag	384
60 Gly Val Leu Ala His Met Leu Leu Ile Cys Arg Phe His Ser Thr Glu	
61 115 120 125	
63 gat cct gaa act gta gat aaa att gtt caa ctt gtt tta cat gaa aag	432

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65		130					135				140						
67	ctg	caa	gat	gct	gta	gga	ccc	cct	aaa	gta	gat	cct	cac	tca	gtt	aaa	480
68	Leu	Gln	Asp	Ala	Val	Gly	Pro	Pro	Lys	Val	Asp	Pro	His	Ser	Val	Lys	
69	145					150					155					160	
71	att	aaa	aaa	atc	aac	aag	aca	gaa	aca	gac	agc	tat	cta	aac	cat	tgc	528
72	Ile	Lys	Lys	Ile	Asn	Lys	Thr	Glu	Thr	Asp	Ser	Tyr	Leu	Asn	His	Cys	
73					165					170					175		
75	tgc	gga	aca	cga	aga	agt	aaa	act	cta	ggg	cag	agt	ctc	agg	atc	gtt	576
76	Cys	Gly	Thr	Arg	Arg	Ser	Lys	Thr	Leu	Gly	Gln	Ser	Leu	Arg	Ile	Val	
77				180					185					190			
79	ggg	ggg	aca	gaa	gta	gaa	gag	ggg	gaa	tgg	ccc	tgg	cag	gct	agc	ctg	624
80	Gly	Gly	Thr	Glu	Val	Glu	Glu	Gly	Glu	Trp	Pro	Trp	Gln	Ala	Ser	Leu	
81		195					200						205				
83	cag	tgg	gat	ggg	agt	cat	gcg	tgt	gga	gca	acc	tta	att	aat	gcc	aca	672
84	Gln	Trp	Asp	Gly	Ser	His	Ala	Cys	Gly	Ala	Thr	Leu	Ile	Asn	Ala	Thr	
85		210					215					220					
87	tgg	ctt	gtg	agt	gct	gct	cac	tgt	ttt	aca	aca	tat	aag	aac	cct	gcc	720
88	Trp	Leu	Val	Ser	Ala	Ala	His	Cys	Phe	Thr	Thr	Tyr	Lys	Asn	Pro	Ala	
89	225				230					235					240		
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92	Arg	Trp	Thr	Ala	Ser	Phe	Gly	Val	Thr	Ile	Lys	Pro	Ser	Lys	Met	Lys	
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95	cgg	ggg	ctc	cgg	aga	ata	att	gtc	cat	gaa	aaa	tac	aaa	cac	cca	tca	816
96	Arg	Gly	Leu	Arg	Arg	Ile	Ile	Val	His	Glu	Lys	Tyr	Lys	His	Pro	Ser	
97			260					265				270					
99	cat	gac	tat	gat	att	tct	ctt	gca	gag	ctt	tct	agc	cct	gtt	ccc	tac	864
100	His	Asp	Tyr	Asp	Ile	Ser	Leu	Ala	Glu	Leu	Ser	Ser	Pro	Val	Pro	Tyr	
101		275						280				285					
103	aca	aat	gca	gta	cat	aga	gtt	tgt	ctc	cct	gat	gca	tcc	tat	gag	ttt	912
104	Thr	Asn	Ala	Val	His	Arg	Val	Cys	Leu	Pro	Asp	Ala	Ser	Tyr	Glu	Phe	
105		290					295					300					
107	caa	cca	ggg	gat	gtg	atg	ttt	gtg	aca	gga	ttt	gga	gca	ctg	aaa	aat	960
108	Gln	Pro	Gly	Asp	Val	Met	Phe	Val	Thr	Gly	Phe	Gly	Ala	Leu	Lys	Asn	
109	305				310					315					320		
111	gat	ggg	tac	agt	caa	aat	cat	ctt	cga	caa	gca	cag	gtg	act	ctc	ata	1008
112	Asp	Gly	Tyr	Ser	Gln	Asn	His	Leu	Arg	Gln	Ala	Gln	Val	Thr	Leu	Ile	
113				325					330					335			
115	gac	gct	aca	act	tgc	aat	gaa	cct	caa	gct	tac	aat	gac	gcc	ata	act	1056
116	Asp	Ala	Thr	Thr	Cys	Asn	Glu	Pro	Gln	Ala	Tyr	Asn	Asp	Ala	Ile	Thr	
117			340						345					350			
119	cct	aga	atc	tta	tgt	gct	ggc	tcc	tta	gaa	gga	aaa	aca	gat	gca	tgc	1104
120	Pro	Arg	Ile	Leu	Cys	Ala	Gly	Ser	Leu	Glu	Gly	Lys	Thr	Asp	Ala	Cys	
121			355				360					365					
123	cag	ggg	gac	tct	gga	gga	cca	ctg	gtt	agt	tca	gat	gct	aga	gat	atc	1152
124	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Ser	Ser	Asp	Ala	Arg	Asp	Ile	
125		370				375						380					
127	tgg	tac	ctt	gct	gga	ata	gtg	agc	tgg	gga	gat	gaa	tgt	gcg	aaa	ccc	1200
128	Trp	Tyr	Leu	Ala	Gly	Ile	Val	Ser	Trp	Gly	Asp	Glu	Cys	Ala	Lys	Pro	

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129 385          390          395          400
131 aac aag cct ggt gtt tat act aga gtt acg gcc ttg cgg gac tgg att      1248
132 Asn Lys Pro Gly Val Tyr Thr Arg Val Thr Ala Leu Arg Asp Trp Ile
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142 <212> TYPE: PRT
143 <213> ORGANISM: DESC1
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152          20          25          30
155 Val Cys Ile Gly Leu Thr Val His Tyr Val Arg Tyr Asn Gln Lys Lys
156          35          40          45
159 Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr Thr Asp Lys Leu Tyr
160          50          55          60
163 Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn Phe Thr Glu Met Ser Gln
164 65          70          75          80
167 Arg Leu Glu Ser Met Val Lys Asn Ala Phe Tyr Lys Ser Pro Leu Arg
168          85          90          95
171 Glu Glu Phe Val Lys Ser Gln Val Ile Lys Phe Ser Gln Gln Lys His
172          100          105          110
175 Gly Val Leu Ala His Met Leu Leu Ile Cys Arg Phe His Ser Thr Glu
176          115          120          125
179 Asp Pro Glu Thr Val Asp Lys Ile Val Gln Leu Val Leu His Glu Lys
180          130          135          140
183 Leu Gln Asp Ala Val Gly Pro Pro Lys Val Asp Pro His Ser Val Lys
184 145          150          155          160
187 Ile Lys Lys Ile Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys
188          165          170          175
191 Cys Gly Thr Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val
192          180          185          190
195 Gly Gly Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu
196          195          200          205
199 Gln Trp Asp Gly Ser His Ala Cys Gly Ala Thr Leu Ile Asn Ala Thr
200          210          215          220
203 Trp Leu Val Ser Ala Ala His Cys Phe Thr Thr Tyr Lys Asn Pro Ala
204 225          230          235          240
207 Arg Trp Thr Ala Ser Phe Gly Val Thr Ile Lys Pro Ser Lys Met Lys
208          245          250          255
211 Arg Gly Leu Arg Arg Ile Ile Val His Glu Lys Tyr Lys His Pro Ser
212          260          265          270
215 His Asp Tyr Asp Ile Ser Leu Ala Glu Leu Ser Ser Pro Val Pro Tyr
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219 Thr Asn Ala Val His Arg Val Cys Leu Pro Asp Ala Ser Tyr Glu Phe

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227 Asp Gly Tyr Ser Gln Asn His Leu Arg Gln Ala Gln Val Thr Leu Ile
228      325      330      335
231 Asp Ala Thr Thr Cys Asn Glu Pro Gln Ala Tyr Asn Asp Ala Ile Thr
232      340      345      350
235 Pro Arg Ile Leu Cys Ala Gly Ser Leu Glu Gly Lys Thr Asp Ala Cys
236      355      360      365
239 Gln Gly Asp Ser Gly Gly Pro Leu Val Ser Ser Asp Ala Arg Asp Ile
240      370      375      380
243 Trp Tyr Leu Ala Gly Ile Val Ser Trp Gly Asp Glu Cys Ala Lys Pro
244 385      390      395      400
247 Asn Lys Pro Gly Val Tyr Thr Arg Val Thr Ala Leu Arg Asp Trp Ile
248      405      410      415
251 Thr Ser Lys Thr Gly Ile
252      420
255 <210> SEQ ID NO: 3
256 <211> LENGTH: 1269
257 <212> TYPE: DNA
258 <213> ORGANISM: DESC1
260 <220> FEATURE:
261 <221> NAME/KEY: CDS
262 <222> LOCATION: (1)..(1269)
263 <223> OTHER INFORMATION:
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271 ccc tgg gtt atc ggc ctc gtc atg ttc ata tcc ctg att gtc ctg gca      96
272 Pro Trp Val Ile Gly Leu Val Met Phe Ile Ser Leu Ile Val Leu Ala
273      20      25      30
275 gtg tgc att gga gtc act gtt cat tat gtg aga tat aat caa aag aag      144
276 Val Cys Ile Gly Val Thr Val His Tyr Val Arg Tyr Asn Gln Lys Lys
277      35      40      45
279 acc tac aat tac tat agc aca ttg tca ttt aca act gac aaa cta tat      192
280 Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr Thr Asp Lys Leu Tyr
281      50      55      60
283 gct gag ttt ggc aga gag gct tct aac aat ttt aca gaa atg agc cag      240
284 Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn Phe Thr Glu Met Ser Gln
285 65      70      75      80
287 aga ctt gaa tca atg gtg aaa aat gca ttt tat aaa tct cca tta agg      288
288 Arg Leu Glu Ser Met Val Lys Asn Ala Phe Tyr Lys Ser Pro Leu Arg
289      85      90      95
291 gaa gaa ttt gtc aag tct cag gtt atc aag ttc agt caa cag aag cat      336
292 Glu Glu Phe Val Lys Ser Gln Val Ile Lys Phe Ser Gln Gln Lys His
293      100      105      110
295 gga gtg ttg gct cat atg ctg ttg att tgt aga ttt cac tct act gag      384
296 Gly Val Leu Ala His Met Leu Leu Ile Cys Arg Phe His Ser Thr Glu

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297	115	120	125	
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304	Leu Gln Asp Ala Val Gly Pro Pro Lys Val Asp Pro His Ser Val Lys			
305	145	150	155	160
307	att aaa aaa atc aac aag aca gaa aca gac agc tat cta aac cat tgc	528		
308	Ile Lys Lys Ile Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys			
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311	tgc gga aca cga aga agt aaa act cta ggt cag agt ctc agg atc gtt	576		
312	Cys Gly Thr Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val			
313	180	185	190	
315	ggt ggg aca gaa gta gaa gag ggt gaa tgg ccc tgg cag gct agc ctg	624		
316	Gly Gly Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu			
317	195	200	205	
319	cag tgg gat ggg agt cat cgc tgt gga gca acc tta att aat gcc aca	672		
320	Gln Trp Asp Gly Ser His Arg Cys Gly Ala Thr Leu Ile Asn Ala Thr			
321	210	215	220	
323	tgg ctt gtg agt gct gct cac tgt ttt aca aca tat aag aac cct gcc	720		
324	Trp Leu Val Ser Ala Ala His Cys Phe Thr Thr Tyr Lys Asn Pro Ala			
325	225	230	235	240
327	aga tgg act gct tcc ttt gga gta aca ata aaa cct tcg aaa atg aaa	768		
328	Arg Trp Thr Ala Ser Phe Gly Val Thr Ile Lys Pro Ser Lys Met Lys			
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332	Arg Gly Leu Arg Arg Ile Ile Val His Glu Lys Tyr Lys His Pro Ser			
333	260	265	270	
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336	His Asp Tyr Asp Ile Ser Leu Ala Glu Leu Ser Ser Pro Val Pro Tyr			
337	275	280	285	
339	aca aat gca gta cat aga gtt tgt ctc cct gat gca tcc tat gag ttt	912		
340	Thr Asn Ala Val His Arg Val Cys Leu Pro Asp Ala Ser Tyr Glu Phe			
341	290	295	300	
343	caa cca ggt gat gtg atg ttt gtg aca gga ttt gga gca ctg aaa aat	960		
344	Gln Pro Gly Asp Val Met Phe Val Thr Gly Phe Gly Ala Leu Lys Asn			
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347	gat ggt tac agt caa aat cat ctt cga caa gca cag gtg act ctc ata	1008		
348	Asp Gly Tyr Ser Gln Asn His Leu Arg Gln Ala Gln Val Thr Leu Ile			
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352	Asp Ala Thr Thr Cys Asn Glu Pro Gln Ala Tyr Asn Asp Ala Ile Thr			
353	340	345	350	
355	cct aga atg tta tgt gct ggc tcc tta gaa gga aaa aca gat gca tgc	1104		
356	Pro Arg Met Leu Cys Ala Gly Ser Leu Glu Gly Lys Thr Asp Ala Cys			
357	355	360	365	
359	cag ggt gac tct gga gga cca ctg gtt agt tca gat gct aga gat atc	1152		
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